



## SEQUENCE LISTING

<110> Kindsvoegel, Wayne R.  
Topouzis, Stavros

<120> SOLUBLE ZCYTOR11 CYTOFLINE RECEPTORS

<130> 00-56

<150> US 60/223,827

<151> 2000-08-08

<150> US 60/250,876

<151> 2000-12-01

<160> 35

<170> FastSEQ for Windows Version 3.0

<210> 1

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<212> DNA

<213> Homo sapien

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<221> CDS

<222> (34)...(1755)

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Leu Thr Val Gly Ser Leu Ala Ala His Ala Pro Glu Asp Pro Ser Asp  
10 15 20

ctg ctg cag cac gtg aaa ttc cag tcc agc aac ttt gaa aac atc ctg 150  
Leu Leu Gln His Val Lys Phe Gln Ser Ser Asn Phe Glu Asn Ile Leu

25	30	35	
acg tgg gac agc ggg cca gag ggc acc cca gac acg gtc tac agc atc			198
Thr Trp Asp Ser Gly Pro Glu Gly Thr Pro Asp Thr Val Tyr Ser Ile			
40	45	50	55
gag tat aag acg tac gga gag agg gac tgg gtg gca aag aag ggc tgt			246
Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp Val Ala Lys Lys Gly Cys			
60	65	70	
cag cgg atc acc cgg aag tcc tgc aac ctg acg gtg gag acg ggc aac			294
Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu Thr Val Glu Thr Gly Asn			
75	80	85	
ctc acg gag ctc tac tat gac agg gtc acc gct gtc agt gcg gga ggc			342
Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr Ala Val Ser Ala Gly Gly			
90	95	100	
cgg tca gcc acc aag atg act gac agg ttc agc tct ctg cag cac act			390
Arg Ser Ala Thr Lys Met Thr Asp Arg Phe Ser Ser Leu Gln His Thr			
105	110	115	
acc ctc aag cca cct gat gtg acc tgt atc tcc aaa gtg aga tcg att			438
Thr Leu Lys Pro Pro Asp Val Thr Cys Ile Ser Lys Val Arg Ser Ile			
120	125	130	135
cag atg att gtt cat cct acc ccc acg cca atc cgt gca ggc gat ggc			486
Gln Met Ile Val His Pro Thr Pro Thr Pro Ile Arg Ala Gly Asp Gly			
140	145	150	
cac cgg cta acc ctg gaa gac atc ttc cat gac ctg ttc tac cac tta			534
His Arg Leu Thr Leu Glu Asp Ile Phe His Asp Leu Phe Tyr His Leu			
155	160	165	
gag ctc cag gtc aac cgc acc tac caa atg cac ctt gga ggg aag cag			582
Glu Leu Gln Val Asn Arg Thr Tyr Gln Met His Leu Gly Gly Lys Gln			
170	175	180	
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Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro Asp Thr Glu Phe Leu Gly			
185	190	195	
acc atc atg att tgc gtt ccc acc tgg gcc aag gag agt gcc ccc tac			678

Thr Ile Met Ile Cys Val Pro Thr Trp Ala Lys Glu Ser Ala Pro Tyr	
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Met Cys Arg Val Lys Thr Leu Pro Asp Arg Thr Trp Thr Tyr Ser Phe	
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Ser Gly Ala Phe Leu Phe Ser Met Gly Phe Leu Val Ala Val Leu Cys	
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tac ctg agc tac aga tat gtc acc aag ccg cct gca cct ccc aac tcc	822
Tyr Leu Ser Tyr Arg Tyr Val Thr Lys Pro Pro Ala Pro Pro Asn Ser	
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ctg aac gtc cag cga gtc ctg act ttc cag ccg ctg cgc ttc atc cag	870
Leu Asn Val Gln Arg Val Leu Thr Phe Gln Pro Leu Arg Phe Ile Gln	
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Glu His Val Leu Ile Pro Val Phe Asp Leu Ser Gly Pro Ser Ser Leu	
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gcc cag cct gtc cag tac tcc cag atc agg gtg tct gga ccc agg gag	966
Ala Gln Pro Val Gln Tyr Ser Gln Ile Arg Val Ser Gly Pro Arg Glu	
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ccc gca gga gct cca cag cgg cat agc ctg tcc gag atc acc tac tta	1014
Pro Ala Gly Ala Pro Gln Arg His Ser Leu Ser Glu Ile Thr Tyr Leu	
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Gly Gln Pro Asp Ile Ser Ile Leu Gln Pro Ser Asn Val Pro Pro Pro	
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Gln Ile Leu Ser Pro Leu Ser Tyr Ala Pro Asn Ala Ala Pro Glu Val	
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Gly Pro Pro Ser Tyr Ala Pro Gln Val Thr Pro Glu Ala Gln Phe Pro	
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Phe Tyr Ala Pro Gln Ala Ile Ser Lys Val Gln Pro Ser Ser Tyr Ala	
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cct caa gcc act ccg gac agc tgg cct ccc tcc tat ggg gta tgc atg	1254
Pro Gln Ala Thr Pro Asp Ser Trp Pro Pro Ser Tyr Gly Val Cys Met	
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Glu Gly Ser Gly Lys Asp Ser Pro Thr Gly Thr Leu Ser Ser Pro Lys	
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His Leu Arg Pro Lys Gly Gln Leu Gln Lys Glu Pro Pro Ala Gly Ser	
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Cys Met Leu Gly Gly Leu Ser Leu Gln Glu Val Thr Ser Leu Ala Met	
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Glu Glu Ser Gln Glu Ala Lys Ser Leu His Gln Pro Leu Gly Ile Cys	
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aca gac aga aca tct gac cca aat gtg cta cac agt ggg gag gaa ggg	1494
Thr Asp Arg Thr Ser Asp Pro Asn Val Leu His Ser Gly Glu Glu Gly	
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atc gag ggc cac ccc atg tcc ctc cct ttg caa cct cct tcc ggt cca	1590
Ile Glu Gly His Pro Met Ser Leu Pro Leu Gln Pro Pro Ser Gly Pro	
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Cys Ser Pro Ser Asp Gln Gly Pro Ser Pro Trp Gly Leu Leu Glu Ser	
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570

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<212> PRT  
<213> Homo sapien

<400> ?

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			20					25					30		
Ser	Asn	Phe	Glu	Asn	Ile	Leu	Thr	Trp	Asp	Ser	Gly	Pro	Glu	Gly	Thr
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Pro	Asp	Thr	Val	Tyr	Ser	Ile	Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp
	50					55					60				
Trp	Val	Ala	Lys	Lys	Gly	Cys	Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn

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Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val						
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Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg						
	100		105		110	
Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys						
	115		120		125	
Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr						
	130		135		140	
Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe						
145		150		155		160
His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln						
	165		170		175	
Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr						
	180		185		190	
Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp						
	195		200		205	
Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp						
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Arg Thr Trp Thr Tyr Ser Phe Ser Gly Ala Phe Leu Phe Ser Met Gly						
225		230		235		240
Phe Leu Val Ala Val Leu Cys Tyr Leu Ser Tyr Arg Tyr Val Thr Lys						
	245		250		255	
Pro Pro Ala Pro Pro Asn Ser Leu Asn Val Gln Arg Val Leu Thr Phe						
	260		265		270	
Gln Pro Leu Arg Phe Ile Gln Glu His Val Leu Ile Pro Val Phe Asp						
	275		280		285	
Leu Ser Gly Pro Ser Ser Leu Ala Gln Pro Val Gln Tyr Ser Gln Ile						
	290		295		300	
Arg Val Ser Gly Pro Arg Glu Pro Ala Gly Ala Pro Gln Arg His Ser						
305		310		315		320
Leu Ser Glu Ile Thr Tyr Leu Gly Gln Pro Asp Ile Ser Ile Leu Gln						
	325		330		335	
Pro Ser Asn Val Pro Pro Pro Gln Ile Leu Ser Pro Leu Ser Tyr Ala						
	340		345		350	
Pro Asn Ala Ala Pro Glu Val Gly Pro Pro Ser Tyr Ala Pro Gln Val						
	355		360		365	
Thr Pro Glu Ala Gln Phe Pro Phe Tyr Ala Pro Gln Ala Ile Ser Lys						
	370		375		380	
Val Gln Pro Ser Ser Tyr Ala Pro Gln Ala Thr Pro Asp Ser Trp Pro						
385		390		395		400
Pro Ser Tyr Gly Val Cys Met Glu Gly Ser Gly Lys Asp Ser Pro Thr						
	405		410		415	

Gly Thr Leu Ser Ser Pro Lys His Leu Arg Pro Lys Gly Gln Leu Gln  
 420 425 430  
 Lys Glu Pro Pro Ala Gly Ser Cys Met Leu Gly Gly Leu Ser Leu Gln  
 435 440 445  
 Glu Val Thr Ser Leu Ala Met Glu Glu Ser Gln Glu Ala Lys Ser Leu  
 450 455 460  
 His Gln Pro Leu Gly Ile Cys Thr Asp Arg Thr Ser Asp Pro Asn Val  
 465 470 475 480  
 Leu His Ser Gly Glu Glu Gly Thr Pro Gln Tyr Leu Lys Gly Gln Leu  
 485 490 495  
 Pro Leu Leu Ser Ser Val Gln Ile Glu Gly His Pro Met Ser Leu Pro  
 500 505 510  
 Leu Gln Pro Pro Ser Gly Pro Cys Ser Pro Ser Asp Gln Gly Pro Ser  
 515 520 525  
 Pro Trp Gly Leu Leu Glu Ser Leu Val Cys Pro Lys Asp Glu Ala Lys  
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<212> PRT

<213> Homo sapiens

<400> 3

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 Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp Trp  
 35 40 45  
 Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn Leu  
 50 55 60  
 Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val Thr  
 65 70 75 80  
 Ala Val Ser Ala Gly Arg Ser Ala Thr Lys Met Thr Asp Arg Phe  
 85 90 95  
 Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys Ile  
 100 105 110  
 Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr Pro  
 115 120 125

Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe His  
 130 135 140  
 Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln Met  
 145 150 155 160  
 His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr Pro  
 165 170 175  
 Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp Ala  
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 Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp Arg  
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 Thr Trp Thr  
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acctctgagg tcacatgctt ggtggtggac gtgagccacg aagacctga ggtcaagttc      180
aactggtacg tggacggcgt ggaggtgcat aatgccaaqa caaagccggg ggaggagcag      240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      300
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cccgtgctgg actccgacgg ctctctcttc ctctacagca agctcaccgt ggacaagagc      600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggtctt gcacaaccac      660
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Leu Met Gly Thr Leu Ala Thr Ser Cys Leu Leu Leu Leu Ala Leu Leu
                   15                   20                   25

gta cag gga gga gca gct gcg ccc atc agc tcc cac tgc agg ctt gac      149
Val Gln Gly Gly Ala Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp
                   30                   35                   40

aag tcc aac ttc cag cag ccc tat atc acc aac cgc acc ttc atg ctg      197
Lys Ser Asn Phe Gln Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu
                   45                   50                   55

gct aag gag gct agc ttg gct gat aac aac aca gac gtt cgt ctc att      245
Ala Lys Glu Ala Ser Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile
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ggg gag aaa ctg ttc cac gga gtc agt atg agt gag cgc tgc tat ctg 293  
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                     80                    85                    90

atg aag cag gtg ctg aac ttc acc ctt gaa gaa gtg ctg ttc cct caa 341  
 Met Lys Gln Val Leu Asn Phe Thr Leu Glu Glu Val Leu Phe Pro Gln  
                     95                    100                    105

tct gat agg ttc cag cct tat atg cag gag gtg gtg ccc ttc ctg gcc 389  
 Ser Asp Arg Phe Gln Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala  
                     110                    115                    120

agg ctc agc aac agg cta agc aca tgt cat att gaa ggt gat gac ctg 437  
 Arg Leu Ser Asn Arg Leu Ser Thr Cys His Ile Glu Gly Asp Asp Leu  
                     125                    130                    135

cat atc cag agg aat gtg caa aag ctg aag gac aca gtg aaa aag ctt 485  
 His Ile Gln Arg Asn Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu  
                     140                    145                    150                    155

gga gag agt gga gag atc aaa gca att gga gaa ctg gat ttg ctg ttt 533  
 Gly Glu Ser Gly Glu Ile Lys Ala Ile Gly Glu Leu Asp Leu Leu Phe  
                     160                    165                    170

atg tct ctg aga aat gcc tgc att tgaccagagc aaagctgaaa aatgaataac 587  
 Met Ser Leu Arg Asn Ala Cys Ile  
                     175

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<212> PRT

<213> homo sapiens

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 Ala Ala Pro Ile Ser Ser His Cys Arg Leu Asp Lys Ser Asn Phe Gln  
 35 40 45  
 Gln Pro Tyr Ile Thr Asn Arg Thr Phe Met Leu Ala Lys Glu Ala Ser  
 50 55 60  
 Leu Ala Asp Asn Asn Thr Asp Val Arg Leu Ile Gly Glu Lys Leu Phe  
 65 70 75 80  
 His Gly Val Ser Met Ser Glu Arg Cys Tyr Leu Met Lys Gln Val Leu  
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 Pro Tyr Met Gln Glu Val Val Pro Phe Leu Ala Arg Leu Ser Asn Arg  
 115 120 125  
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 130 135 140  
 Val Gln Lys Leu Lys Asp Thr Val Lys Lys Leu Gly Glu Ser Gly Glu  
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 Ala Cys Ile

&lt;210&gt; 9

&lt;211&gt; 36

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide prime ZC28590

&lt;400&gt; 9

ttgggtacct ctgcaatggc cgcctgcag aaatct

36

&lt;210&gt; 10

&lt;211&gt; 33

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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<212> DNA

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&lt;223&gt; Oligonucleotide primer ZC29239

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&lt;210&gt; 15

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&lt;223&gt; Oligonucleotide primer ZC29232

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&lt;213&gt; Artificial Sequence

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&lt;223&gt; Oligonucleotide primer ZC39319

&lt;400&gt; 16

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&lt;210&gt; 17

&lt;211&gt; 28

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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&lt;223&gt; Oligonucleotide primer ZC39325

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 <222> (1)...(660)

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1				5				10				15				

gca	ttg	gga	atg	gla	cca	cct	ccc	gaa	aat	gtc	aga	atg	aat	tct	gtt	96
Ala	Leu	Gly	Met	Val	Pro	Pro	Pro	Glu	Asn	Val	Arg	Met	Asn	Ser	Val	
			20					25				30				

aat	ttc	aag	aac	att	cta	cag	tgg	gag	tca	cct	gct	ttt	gcc	aaa	ggg	144
Asn	Phe	Lys	Asn	Ile	Leu	Gln	Trp	Glu	Ser	Pro	Ala	Phe	Ala	Lys	Gly	
		35					40					45				

aac	ctg	act	ttc	aca	gct	cag	tac	cta	agt	tat	agg	ata	ttc	caa	gat	192
Asn	Leu	Thr	Phe	Thr	Ala	Gln	Tyr	Leu	Ser	Tyr	Arg	Ile	Phe	Gln	Asp	
	50					55					60					

aaa	tgc	atg	aat	act	acc	ttg	acg	gaa	tgt	gat	ttc	tca	agt	ctt	tcc	240
Lys	Cys	Met	Asn	Thr	Thr	Leu	Thr	Glu	Cys	Asp	Phe	Ser	Ser	Leu	Ser	
65					70				75					80		

aag	tat	ggg	gac	cac	acc	ttg	aga	gtc	agg	gct	gaa	ttt	gca	gat	gag	288
Lys	Tyr	Gly	Asp	His	Thr	Leu	Arg	Val	Arg	Ala	Glu	Phe	Ala	Asp	Glu	
			85					90					95			

cat	tca	gac	tgg	gta	aac	atc	acc	ttc	tgt	cct	gtg	gat	gac	acc	att	336
His	Ser	Asp	Trp	Val	Asn	Ile	Thr	Phe	Cys	Pro	Val	Asp	Asp	Thr	Ile	
			100					105					110			

att	gga	ccc	cct	gga	atg	caa	gta	gaa	gta	ctt	gat	gat	tct	tta	cat	384
Ile	Gly	Pro	Pro	Gly	Met	Gln	Val	Glu	Val	Leu	Asp	Asp	Ser	Leu	His	
	115					120					125					

atg	cgt	ttc	tta	gac	cct	aaa	att	gag	aat	gaa	tac	gaa	act	tgg	act	432
Met	Arg	Phe	Leu	Ala	Pro	Lys	Ile	Glu	Asn	Glu	Tyr	Glu	Thr	Trp	Thr	

130	135	140	
atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa			480
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys			
145	150	155	160
aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag			528
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu			
165	170	175	
gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga			576
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Lys Val Gln Val Arg			
180	185	190	
ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc			624
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val			
195	200	205	
tgt gag caa aca acc cat gac gaa acg gtc ccc tcc			660
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser			
210	215	220	

&lt;210&gt; 19

&lt;211&gt; 220

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 19

Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser			
1	5	10	15
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val			
20	25	30	
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly			
35	40	45	
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp			
50	55	60	
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser			
65	70	75	80
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu			
85	90	95	
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile			
100	105	110	

Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His  
           115                          120                          125  
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr  
       130                          135                          140  
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys  
 145                          150                          155                          160  
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu  
                           165                          170                          175  
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg  
                           180                          185                          190  
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val  
       195                          200                          205  
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser  
       210                          215                          220

&lt;210&gt; 20

&lt;211&gt; 18

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC38931

&lt;400&gt; 20

acaaagccgc gggaggag

18

&lt;210&gt; 21

&lt;211&gt; 82

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC39042

&lt;400&gt; 21

ctgactcgag ttagtgatgg tgatggtgat ggccacctga tccggaacca cgcggaacca  
 gttaccctgg agacaggag ag

60

82

&lt;210&gt; 22

&lt;211&gt; 1428

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence



&lt;210&gt;

&lt;211&gt; CDS

&lt;212&gt; (1)...(1428)

<213> (RF2-4 extracellular cytokine binding domain fused  
to IgG1 with a 6-HIS tag)

&lt;400&gt; 22

atg gca tgg agt ctt ggg agc tgg ctg ggt ggc tgc ctg ctg gtg tca	48
Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser	
1 5 10 15	
gca ttg gga atg gta cca cct ccc gaa aat gtc aga atg aat tct gtt	96
Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val	
20 25 30	
aat ttc aag aac att cta cag tgg gag tca cct gct ttt gcc aaa ggg	144
Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly	
35 40 45	
aac ctg act ttc aca gct cag tac cta agt tat agg ata ttc caa gat	192
Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp	
50 55 60	
aaa tgc atg aat act acc ttg acg gaa tgt gat ttc tca agt ctt tcc	240
Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser	
65 70 75 80	
aag tat ggt gac cac acc ttg aga gtc agg gct gaa ttt gca gat gag	288
Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu	
85 90 95	
cat tca gac tgg gta aac atc acc ttc tgt cct gtg gat gac acc att	336
His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile	
100 105 110	
att gga ccc cct gga atg caa gta gaa gta ctt gat gat tct tta cat	384
Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His	
115 120 125	
atg cgt ttc tta gcc cct aaa att gag aat gaa tac gaa act tgg act	432
Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr	
130 135 140	

atg aag aat gtg tat aac tca tgg act tat aat gtg caa tac tgg aaa	480
Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys	
145 150 155 160	
aac ggt act gat gaa aag ttt caa att act ccc cag tat gac ttt gag	518
Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu	
165 170 175	
gtc ctc aga aac ctg gag cca tgg aca act tat tgt gtt caa gtt cga	576
Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg	
180 185 190	
ggg ttt ctt cct gat cgg aac aaa gct ggg gaa tgg agt gag cct gtc	624
Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val	
195 200 205	
tgt gag caa aca acc cat gac gaa acg gtc ccc tcc gga tcc ggt tgg	672
Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser	
210 215 220	
ggt tgg ggt tgg gag ccc aga tca tca gac aaa act cac aca tgc cca	720
Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro	
225 230 235 240	
ccg tgc cca gca cct gaa gcc gag ggg gca ccg tca gtc ttc ctc ttc	768
Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe	
245 250 255	
ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc	816
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val	
260 265 270	
aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc	864
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe	
275 280 285	
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg	912
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro	
290 295 300	
cgg gag gag cag tac aac agc aag tac cgt gtg gtc agc gtc ctc acc	960
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr	

305	310	315	320	
gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc				1008
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val				
	325	330	335	
tec aac aaa gcc ctc cca tcc tcc atc gag aaa acc atc tcc aaa gcc				1056
Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala				
	340	345	350	
aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg				1104
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg				
	355	360	365	
gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc				1152
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly				
	370	375	380	
ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg				1200
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro				
	385	390	395	400
gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc				1248
Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser				
	405	410	415	
ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag				1296
Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln				
	420	425	430	
ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac				1344
Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His				
	435	440	445	
tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa ctg gtt ccg cgt				1392
Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg				
	450	455	460	
ggt tcc gga tca ggt ggc cat cac cat cac cat cac				1428
Gly Ser Gly Ser Gly Gly His His His His His His				
	465	470	475	

&lt;210&gt; 23

&lt;211&gt; 476

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 23

Met Ala Trp Ser Leu Gly Ser Trp Leu Gly Gly Cys Leu Leu Val Ser  
 1 5 10 15  
 Ala Leu Gly Met Val Pro Pro Pro Glu Asn Val Arg Met Asn Ser Val  
 20 25 30  
 Asn Phe Lys Asn Ile Leu Gln Trp Glu Ser Pro Ala Phe Ala Lys Gly  
 35 40 45  
 Asn Leu Thr Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp  
 50 55 60  
 Lys Cys Met Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser  
 65 70 75 80  
 Lys Tyr Gly Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu  
 85 90 95  
 His Ser Asp Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile  
 100 105 110  
 Ile Gly Pro Pro Gly Met Gln Val Glu Val Leu Asp Asp Ser Leu His  
 115 120 125  
 Met Arg Phe Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr  
 130 135 140  
 Met Lys Asn Val Tyr Asn Ser Trp Thr Tyr Asn Val Glu Tyr Trp Lys  
 145 150 155 160  
 Asn Gly Thr Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu  
 165 170 175  
 Val Leu Arg Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg  
 180 185 190  
 Gly Phe Leu Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val  
 195 200 205  
 Cys Glu Gln Thr Thr His Asp Glu Thr Val Pro Ser Gly Ser Gly Ser  
 210 215 220  
 Gly Ser Gly Ser Glu Pro Arg Ser Ser Asp Lys Thr His Thr Cys Pro  
 225 230 235 240  
 Pro Cys Pro Ala Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe  
 245 250 255  
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val  
 260 265 270  
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe  
 275 280 285  
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro

290                      295                      300  
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr  
 305                      310                      315                      320  
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val  
                     325                      330                      335  
 Ser Asn Lys Ala Leu Pro Ser Ser Ile Glu Lys Thr Ile Ser Lys Ala  
                     340                      345                      350  
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
                     355                      360                      365  
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
                     370                      375                      380  
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro  
 385                      390                      395                      400  
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser  
                     405                      410                      415  
 Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln  
                     420                      425                      430  
 Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His  
                     435                      440                      445  
 Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys Leu Val Pro Arg  
                     450                      455                      460  
 Gly Ser Gly Ser Gly Gly His His His His His His  
 465                      470                      475

&lt;210&gt; 24

&lt;211&gt; 63

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC29328

&lt;400&gt; 24

tcagaggaat cgggttcggg ttgggttcg gagccagat catcagacaa aactcacaca  
 tgc

60

63

&lt;210&gt; 25

&lt;211&gt; 65

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC29231

<400> 25  
 cgactgactc gagctactcc ataggcatat actcgccacc tgatccttta cccggagaca 60  
 gggag 65

<210> 26  
 <211> 70  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC39335

<400> 26  
 atcggaaftc gcagaagcca tgaggacgct gctgaccatc ttgactgtgg ggtccctggc 60  
 tgctcacgcc 70

<210> 27  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC28981

<400> 27  
 ttgggctcc ctgagctctg gtggaa 26

<210> 28  
 <211> 80  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC39043

<400> 28  
 ctgactgag ctactccata ggcataact cgccacctga tccggaacca cgcggaacca 60  
 gttaccggg apacagggag 80

<210> 29  
 <211> 1452  
 <212> DNA

## &lt;13&gt; Artificial Sequence

&lt;20&gt;

<23> h:cytor11 extracellular cytokine binding domain  
fused to IgGg1 with a Glu-Glu tag

&lt;271&gt; CDS

&lt;222&gt; (1)...(1452)

&lt;400&gt; 29

atg	agg	acg	ctg	ctg	acc	atc	ttg	act	gtg	gga	tcc	ctg	gct	gct	cac	48
Met	Arg	Thr	Leu	Leu	Thr	Ile	Leu	Thr	Val	Gly	Ser	Leu	Ala	Ala	His	
1			5				10				15					

gcc	cct	gag	gac	ccc	tgg	gat	ctg	ctc	cag	cac	gtg	aaa	ttc	cag	tcc	96
Ala	Pro	Glu	Asp	Pro	Ser	Asp	Leu	Leu	Gln	His	Val	Lys	Phe	Gln	Ser	
		20					25				30					

agc	aac	ttt	gaa	aac	atc	ctg	acg	tgg	gac	agc	ggg	cca	gag	ggc	acc	144
Ser	Asn	Phe	Glu	Asn	Ile	Leu	Thr	Trp	Asp	Ser	Gly	Pro	Glu	Gly	Thr	
	35					40					45					

cca	gac	acg	gtc	tac	agc	atc	gag	tat	aag	acg	tac	gga	gag	agg	gac	192
Pro	Asp	Thr	Val	Tyr	Ser	Ile	Glu	Tyr	Lys	Thr	Tyr	Gly	Glu	Arg	Asp	
	50					55					60					

tgg	gtg	gca	aag	aag	ggc	tgt	cag	cgg	atc	acc	cgg	aag	tcc	tgc	aac	240
Trp	Val	Ala	Lys	Lys	Gly	Cys	Gln	Arg	Ile	Thr	Arg	Lys	Ser	Cys	Asn	
65					70				75					80		

ctg	acg	gtg	gag	acg	ggc	aac	ctc	acg	gag	ctc	tac	tat	gcc	agg	gtc	288
Leu	Thr	Val	Glu	Thr	Gly	Asn	Leu	Thr	Glu	Leu	Tyr	Tyr	Ala	Arg	Val	
			85						90				95			

acc	gct	gtc	agt	ggc	gga	ggc	cgg	tca	gcc	acc	aag	atg	act	gac	agg	336
Thr	Ala	Val	Ser	Ala	Gly	Gly	Arg	Ser	Ala	Thr	Lys	Met	Thr	Asp	Arg	
			100				105					110				

ttc	agc	tct	ctg	cag	cac	act	acc	ctc	aag	cca	cct	gat	gtg	acc	tgt	384
Phe	Ser	Ser	Leu	Gln	His	Thr	Thr	Leu	Lys	Pro	Pro	Asp	Val	Thr	Cys	
	115					120						125				

atc	tcc	aaa	gtg	aga	tgg	att	cag	atg	att	gtt	cat	cct	acc	ccc	acg	432
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Ile	Ser	Lys	Val	Arg	Ser	Ile	Gln	Met	Ile	Val	His	Pro	Thr	Pro	Thr	
130						135						140				
cca	atc	cgt	gca	ggc	gat	ggc	cac	cgg	cta	acc	ctg	gaa	gac	atc	ttc	480
Pro	Ile	Arg	Ala	Gly	Asp	Gly	His	Arg	Leu	Thr	Leu	Glu	Asp	Ile	Phe	
145						150						155				160
cat	gac	ctg	ttc	tac	cac	tta	gag	ctc	cag	gtc	aac	cgc	acc	tac	caa	528
His	Asp	Leu	Phe	Tyr	His	Leu	Glu	Leu	Gln	Val	Asn	Arg	Thr	Tyr	Gln	
				165						170					175	
atg	cac	ctt	gga	ggg	aag	cag	aga	gaa	tat	gag	ttc	ttc	ggc	ctg	acc	576
Met	His	Leu	Gly	Gly	Lys	Gln	Arg	Glu	Tyr	Glu	Phe	Phe	Gly	Leu	Thr	
			180					185					190			
cct	gac	aca	gag	ttc	ctt	ggc	acc	atc	atg	att	tgc	gtt	ccc	acc	tgg	624
Pro	Asp	Thr	Glu	Phe	Leu	Gly	Thr	Ile	Met	Ile	Cys	Val	Pro	Thr	Trp	
			195				200					205				
gcc	aag	gag	agt	gcc	ccc	tac	atg	tgc	cga	gtg	aag	aca	ctg	cca	gac	672
Ala	Lys	Glu	Ser	Ala	Pro	Tyr	Met	Cys	Arg	Val	Lys	Thr	Leu	Pro	Asp	
210						215						220				
cgg	aca	tgg	acc	gga	tcc	ggt	tcg	ggt	tcg	ggt	tcg	gag	ccc	aga	tca	720
Arg	Thr	Trp	Thr	Gly	Ser	Gly	Ser	Gly	Ser	Gly	Ser	Glu	Pro	Arg	Ser	
225					230					235					240	
tca	gac	aaa	act	cac	aca	tgc	cca	ccg	tgc	cca	gca	cct	gaa	gcc	gag	768
Ser	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala	Glu	
				245					250					255		
ggg	gca	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	ctc	816
Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	
			260				265						270			
atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	agc	864
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	
275							280					285				
cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	gag	912
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	
290						295					300					



gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg	960
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr	
305 310 315 320	
tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat	1008
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn	
325 330 335	
ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca tcc tcc	1056
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser	
340 345 350	
atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag	1104
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln	
355 360 365	
gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc	1152
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val	
370 375 380	
agc ctg acc tgc ctg gtc aaa gcc ttc tat ccc agc gac atc gcc gtg	1200
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val	
385 390 395 400	
gag tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct	1248
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro	
405 410 415	
ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc	1296
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr	
420 425 430	
gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg	1344
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val	
435 440 445	
atg cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg	1392
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu	
450 455 460	
tct ccg ggt aaa ctg gtt ccg cgt ggt tcc qqa tca ggt qgc qag tat	1440
Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Gly Glu Tyr	
465 470 475 480	

atg cct atg gag  
Met Pro Met Glu

1452

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<211> 484  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> hzcytor11 extracellular cytokine binding domain  
fused to IgG1 with a Glu-Glu tag

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1 5 10 15  
Ala Pro Glu Asp Pro Ser Asp Leu Leu Gln His Val Lys Phe Gln Ser  
20 25 30  
Ser Asn Phe Glu Asn Ile Leu Thr Trp Asp Ser Gly Pro Glu Gly Thr  
35 40 45  
Pro Asp Thr Val Tyr Ser Ile Glu Tyr Lys Thr Tyr Gly Glu Arg Asp  
50 55 60  
Trp Val Ala Lys Lys Gly Cys Gln Arg Ile Thr Arg Lys Ser Cys Asn  
65 70 75 80  
Leu Thr Val Glu Thr Gly Asn Leu Thr Glu Leu Tyr Tyr Ala Arg Val  
85 90 95  
Thr Ala Val Ser Ala Gly Gly Arg Ser Ala Thr Lys Met Thr Asp Arg  
100 105 110  
Phe Ser Ser Leu Gln His Thr Thr Leu Lys Pro Pro Asp Val Thr Cys  
115 120 125  
Ile Ser Lys Val Arg Ser Ile Gln Met Ile Val His Pro Thr Pro Thr  
130 135 140  
Pro Ile Arg Ala Gly Asp Gly His Arg Leu Thr Leu Glu Asp Ile Phe  
145 150 155 160  
His Asp Leu Phe Tyr His Leu Glu Leu Gln Val Asn Arg Thr Tyr Gln  
165 170 175  
Met His Leu Gly Gly Lys Gln Arg Glu Tyr Glu Phe Phe Gly Leu Thr  
180 185 190  
Pro Asp Thr Glu Phe Leu Gly Thr Ile Met Ile Cys Val Pro Thr Trp  
195 200 205  
Ala Lys Glu Ser Ala Pro Tyr Met Cys Arg Val Lys Thr Leu Pro Asp

210	215	220
Arg Thr Trp Thr Gly Ser Gly Ser Gly Ser Gly Ser Glu Pro Arg Ser		
225	230	235 240
Ser Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu		
	245	250 255
Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu		
	260	265 270
Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser		
	275	280 285
His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu		
	290	295 300
Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr		
305	310	315 320
Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn		
	325	330 335
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ser Ser		
	340	345 350
Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln		
	355	360 365
Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val		
	370	375 380
Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val		
385	390	395 400
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro		
	405	410 415
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr		
	420	425 430
Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val		
	435	440 445
Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu		
	450	455 460
Ser Pro Gly Lys Leu Val Pro Arg Gly Ser Gly Ser Gly Gly Glu Tyr		
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Met Pro Met Glu		

<210> 31

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC37693

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22

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<220>  
<223> Oligonucleotide primer ZC37449

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23

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<212> PRT  
<213> Homo sapiens

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Phe Thr Ala Gln Tyr Leu Ser Tyr Arg Ile Phe Gln Asp Lys Cys Met  
35 40 45  
Asn Thr Thr Leu Thr Glu Cys Asp Phe Ser Ser Leu Ser Lys Tyr Gly  
50 55 60  
Asp His Thr Leu Arg Val Arg Ala Glu Phe Ala Asp Glu His Ser Asp  
65 70 75 80  
Trp Val Asn Ile Thr Phe Cys Pro Val Asp Asp Thr Ile Ile Gly Pro  
85 90 95  
Pro Gly Met Gln Val Glu Val Leu Ala Asp Ser Leu His Met Arg Phe  
100 105 110  
Leu Ala Pro Lys Ile Glu Asn Glu Tyr Glu Thr Trp Thr Met Lys Asn  
115 120 125  
Val Tyr Asn Ser Trp Thr Tyr Asn Val Gln Tyr Trp Lys Asn Gly Thr  
130 135 140  
Asp Glu Lys Phe Gln Ile Thr Pro Gln Tyr Asp Phe Glu Val Leu Arg  
145 150 155 160  
Asn Leu Glu Pro Trp Thr Thr Tyr Cys Val Gln Val Arg Gly Phe Leu  
165 170 175

Pro Asp Arg Asn Lys Ala Gly Glu Trp Ser Glu Pro Val Cys Glu Gln  
                   180                  185                  190  
 Thr Thr His Asp Glu Thr Val  
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<210> 34

<211> 211

<212> PRT

<213> Homo sapiens

<400> 34

Ser Asp Ala His Gly Thr Glu Leu Pro Ser Pro Pro Ser Val Trp Phe  
   1                  5                  10                  15  
 Glu Ala Glu Phe Phe His His Ile Leu His Trp Thr Pro Ile Pro Asn  
                   20                  25                  30  
 Gln Ser Glu Ser Thr Cys Tyr Glu Val Ala Leu Leu Arg Tyr Gly Ile  
                   35                  40                  45  
 Glu Ser Trp Asn Ser Ile Ser Asn Cys Ser Gln Thr Leu Ser Tyr Asp  
                   50                  55                  60  
 Leu Thr Ala Val Thr Leu Asp Leu Tyr His Ser Asn Gly Tyr Arg Ala  
  65                  70                  75                  80  
 Arg Val Arg Ala Val Asp Gly Ser Arg His Ser Asn Trp Thr Val Thr  
                   85                  90                  95  
 Asn Thr Arg Phe Ser Val Asp Glu Val Thr Leu Thr Val Gly Ser Val  
                  100                 105                 110  
 Asn Leu Glu Ile His Asn Gly Phe Ile Leu Gly Lys Ile Gln Leu Pro  
                  115                 120                 125  
 Arg Pro Lys Met Ala Pro Ala Asn Asp Thr Tyr Glu Ser Ile Phe Ser  
                  130                 135                 140  
 His Phe Arg Glu Tyr Glu Ile Ala Ile Arg Lys Val Pro Gly Asn Phe  
  145                 150                 155                 160  
 Thr Phe Thr His Lys Lys Val Lys His Glu Asn Phe Ser Leu Leu Thr  
                  165                 170                 175  
 Ser Gly Glu Val Gly Glu Phe Cys Val Gln Val Lys Pro Ser Val Ala  
                  180                 185                 190  
 Ser Arg Ser Asn Lys Gly Met Trp Ser Lys Glu Glu Cys Ile Ser Leu  
                  195                 200                 205  
 Thr Arg Gln  
                  210

<210> 35

<211> 201

<212> PRT

<213> Homo sapiens

&lt;400&gt; 35

Asp 1	Glu	Val	Ala	Ile 5	Leu	Pro	Ala	Pro	Gln 10	Asn	Leu	Ser	Val	Leu 15	Ser
Thr	Asn	Met	Lys	His	Leu	Leu	Met	Trp	Ser	Pro	Val	Ile	Ala	Pro	Gly
			20					25					30		
Glu	Thr	Val	Tyr	Tyr	Ser	Val	Glu	Tyr	Gln	Gly	Glu	Tyr	Glu	Ser	Leu
		35					40					45			
Tyr	Thr	Ser	His	Ile	Trp	Ile	Pro	Ser	Ser	Trp	Cys	Ser	Leu	Thr	Glu
	50					55					60				
Gly	Pro	Glu	Cys	Asp	Val	Thr	Asp	Asp	Ile	Thr	Ala	Thr	Val	Pro	Tyr
65					70					75					80
Asn	Leu	Arg	Val	Arg	Ala	Thr	Leu	Gly	Ser	Gln	Thr	Ser	Ala	Trp	Ser
			85					90						95	
Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser	Thr	Ile	Leu	Thr	Arg	Pro
			100					105					110		
Gly	Met	Glu	Ile	Thr	Lys	Asp	Gly	Phe	His	Leu	Val	Ile	Glu	Leu	Glu
		115					120					125			
Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe	Leu	Val	Ala	Tyr	Trp	Arg	Arg	Glu
	130					135				140					
Pro	Gly	Ala	Glu	Glu	His	Val	Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro
145					150					155					160
Val	His	Leu	Glu	Thr	Met	Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala
			165						170					175	
Gln	Thr	Phe	Val	Lys	Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr
		180						185					190		
Glu	Cys	Val	Glu	Val	Gln	Gly	Glu	Ala							
		195					200								